

Figure 1

	10	20	30	40	50
XYN2_TRIRE	---	MVSFTSLLAASPP-SRASC	RPAAEV---	ESVAVEKRQTIQ----	P
XYN1_HUMIN	---	MVSLKSVLAAATAVSSAIAAP	FDVPRDNSTALQARQVTP----	N	
XYNA_BACST	-----	MKLKKKMLTLLLTASMSFGLF----	G		
XYN1_TRIRE	---	MVAFSSLICALTSIASTLAMPTGLE	PESSVNVTERGMYDFVLGAHND		
XYN1_ASPAW	-----	MKVTAAFAGLLVTAFAPVPEPVLVS----			
XYN2_BACST	MCSSIPSLREVFANDFRIGA	AVNPVTLEAQQSLLIRHVNSLTAENHMKFE			

	60	70	80	90	100
XYN2_TRIRE	GTGYNNGYFY	SYWNDGHGGV	TYTNGPGGQFSVNWS--	NSG-NFVGKGKQWQ	
XYN1_HUMIN	AEGWHNGYFY	SWSDGGGQVQYTNLEGSRYQVRWR--	NTG-NFVGKGKWN		
XYNA_BACST	ATSSAATDYWQY	WTDGGGMVNAVNGPGGNYSVTWQ--	NTG-NFVGKGKWT		
XYN1_TRIRE	HRRRASINYDQNY	QTG-GQVSYSPSNTG-FSVNWN--	TQD-DFVVGVGWT		
XYN1_ASPAW	--RSAGINYVQNY	NGNLGDFTYDESAGT-FSMYWEDGVSS-DFVVGGLGWT			
XYN2_BACST	HLQPEEGRFTFDIAIKS	STSPFSSHGVRGHTLVWHNQTPSWVPQDSQGHF			

	110	120	130	140	150
XYN2_TRIRE	PGTKNKVINFS-GSYNPNGNSYLSVYGWSRNPLIEYYIVENF---	GTYNP			
XYN1_HUMIN	PGT-GRITINYG-GYFNPQNGYLAVYGWTRNPLVEYYVIESY---	GTYNP			
XYNA_BACST	VGSPNRVINYNAGIWEPSGNGYLTLYGWTRNALIEYYVVDSW---	GTYP			
XYN1_TRIRE	TGS-SAPINFGGSFSVNSGTGLLSVYGWSTNPLVEYYIMED-----	NHNY			
XYN1_ASPAW	TGS-SNAITYSAEYSASGSSSYLAVYGWVNYPPQAEYYIVEDY---	GDYNP			
XYN2_BACST	VGRDVLLERMKSHISTVVQRYKGKVYCWDVINEA VADEGSEWLRSSTWRQ				

	160	170	180	190	200
XYN2_TRIRE	STGATKLGEVTS	SDGSVYDIYRTQ	RVNQPSII	GTATFYQYWSVRRNHRSSG	
XYN1_HUMIN	GSQAQYKGTFTY	TDGDQYDIFVSTRYNQPSIDG	TRTFQYQYWSIRKNKRVGG		
XYNA_BACST	T--GNYKGTVNSDGGTY	DIYTTMRYNAPSIDGTQTFQQFWSVRQSKRPTG			
XYN1_TRIRE	PAQGTVKGTVTS	SDGATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTSG			
XYN1_ASPAW	CSSATSLGTVYSDGSTYQVCTD	TRTNEPSITGTSTFTQYFSVRESTRTSG			
XYN2_BACST	IIGDDFIQQAFLYAHEADPEALLFYNDYNECFPEKREKIYTLVKSLRDKG				

Figure 1

	210	220	230	240	250
XYN2_TRIRE	S----	VNTANHFNAWA-QQGLTLGTMD-YQIVAVEGYFSSGSASITVS--			
XYN1_HUMIN	S----	VNMQNHFNWQ-QHGMPLGQHY-YQVVATEGYQSSGESDIYVQTH			
XYNA_BACST	SNV-SITFSNHVNAWR-SKGMNLGSSWAYQVLATEGYQSSGRSNVTW--				
XYN1_TRIRE	T----	VTQNHFNWAW-SLGLHLGQMN-YQVVAVEGWGGSGSASQSVSN-			
XYN1_ASPAW	T----	VTVANHFNFWA-QHGFNGSDFN-YQVMAVEAWSGAGSASVTISS-			
XYN2_BACST	IPIHGIGMQAHWSLNRPTLDEIRAAIERYASLGVILHITELDISMFEFDD				

	260	270	280	290	300
XYN2_TRIRE	-----				

Figure 1

XYN1_HUMIN	-----
XYN1_BACST	-----
XYN1_TRIRE	-----
XYN1_ASPAW	-----
XYN2_BACST	HRKDLAAPTNEVERQAERYEQIFSLFKEYRDVIONVTFWGIADDHTWLD

	310	320	330
XYN2_TRIRE			
XYN1_HUMIN	-----	-----	-----
XYN1_BACST	-----	-----	-----
XYN1_TRIRE	-----	-----	-----
XYN1_ASPAW	-----	-----	-----
XYN2_BACST	HFPVQGRKNWPLLFD	EQHNPKPAFWRVVNI	

[illegible]

Figure 3

H22K	5'- GAACGATGGCAAGGGCGGCGTGACG -3'
S65C	5'- CTTCTCGGGCTGCTACAACCCAAACGG -3'
N92C	5'- ACATCGTCGAGTGTTTTGGCACCTAC -3'
F93W	5'- CATCGTCGAGAACTGGGGCACCTACAACC -3'
N97R	5'- GGCACCTACCGACCGTCCACG -3'
V108H	5'- CAAGCTGGGCGAGCACACCTCCGAC -3'
H144C	5'- CGCCGCAACTGTCGCTCGAGC -3'
F180Q	5'- GTGGAGGGTTACCAAAGCTCTGGCTCTGC -3'
S186C	5'- TCTGGCTCTGCTTGCATACCGTCAGC -3'
T2C	5'-GAGAAGCGCCAGTGCATTAGCCCGGC-3'
T28C	5'-GTGACGTACTGCAATGGTCCCGGCGGG-3'
K58R	5'-GGCACCAAGAACAGGGTCATCAACTTCTCGGGC-3'
191D	5'-TCCATCACCGTCAGCGATTAAAGGGGGCTCTTC-3'
P5C	5'-CCCAGACGATTAGTGCGGCACGGGCTACAAC-3'
N19C	5'-CTTCTACTCGTACTGGTGCGATGGCCACGGCG-3'
T7C	5'-CGATTAGCCCGGCTGCGGCTACAACAACGGC-3'
S16C	5'-CAACGGCTACTTCTACTGCTACTGGAACGATGGCC-3'
N10C	5'-CCGGCACGGGCTACTGCAACGGCTACTTCTACTC-3'
N29C	5'-GGCGTGACGTACACCTGCGGTCCCGGCGGGC-3'
L105C	5'-GGCGCCACCAAGTGCGGCGAGGTCACC-3'
Q162C	5'-GCGTGGGCTCAGTGCGGCCTGACGCTCG-3'

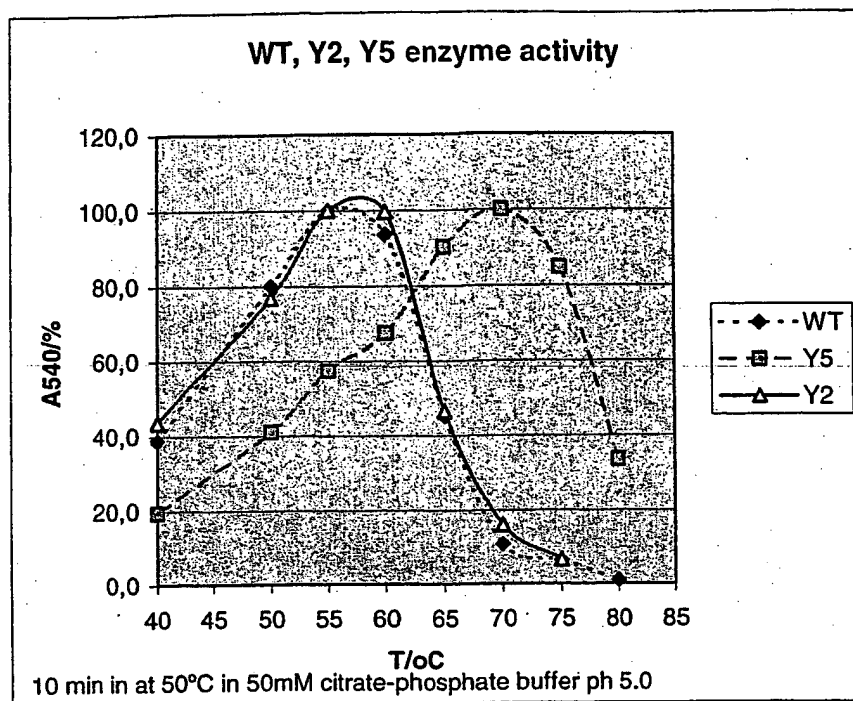
Figure 4.

Figure 5

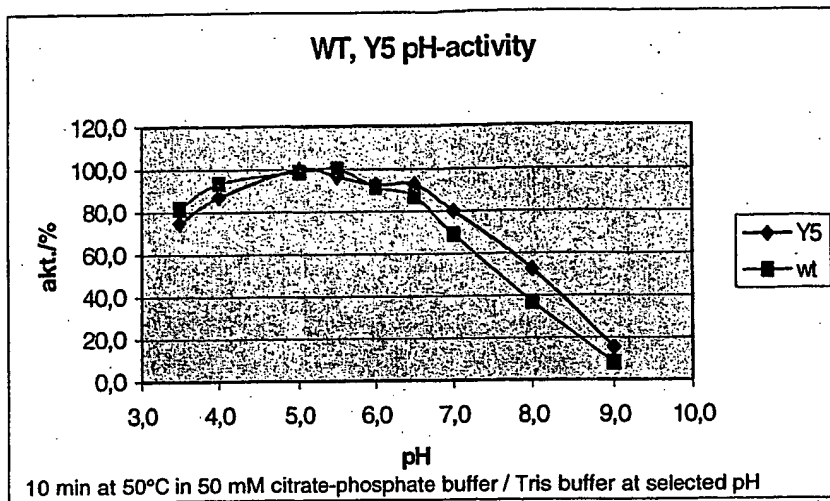


Figure 6

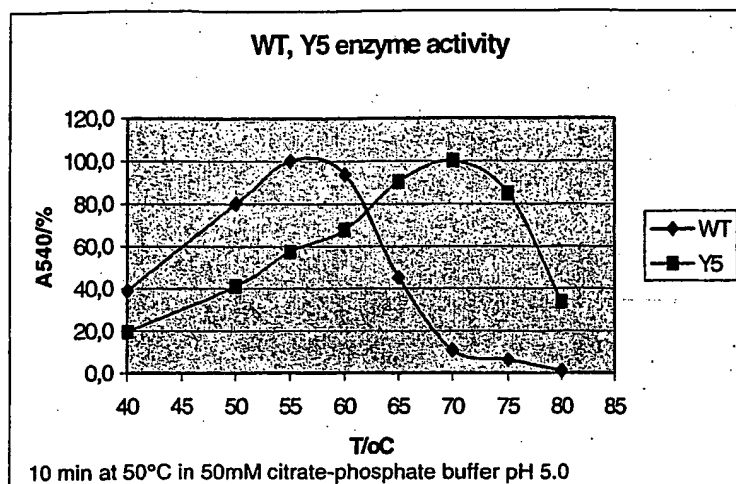


Figure 7

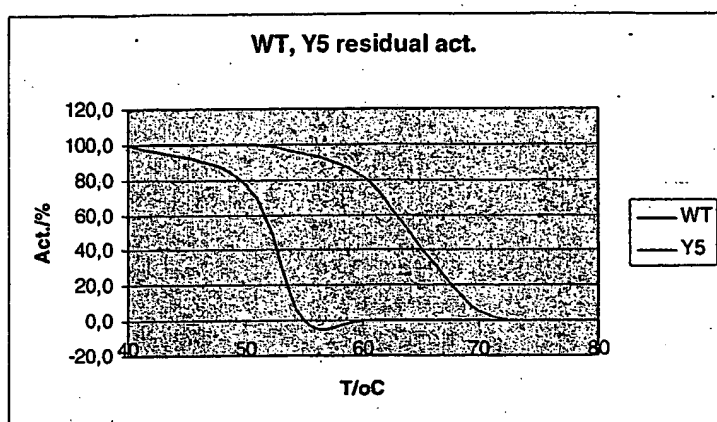


Figure 8

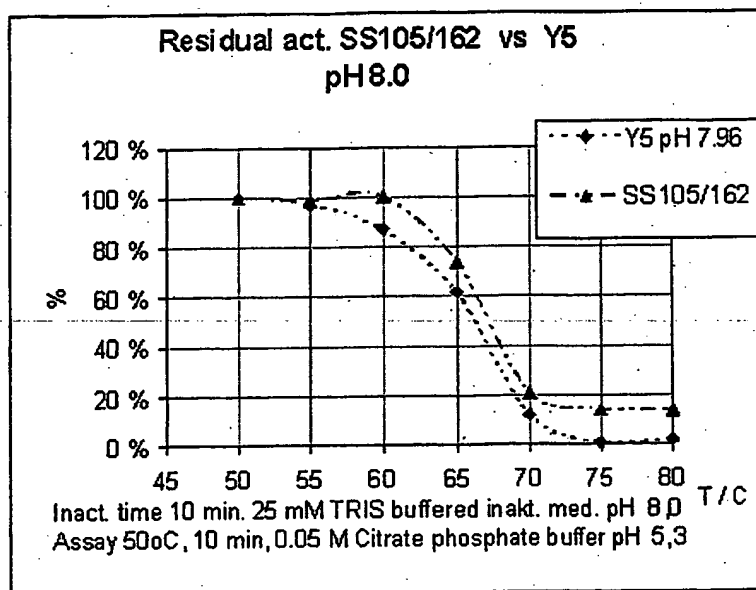


Figure 9.

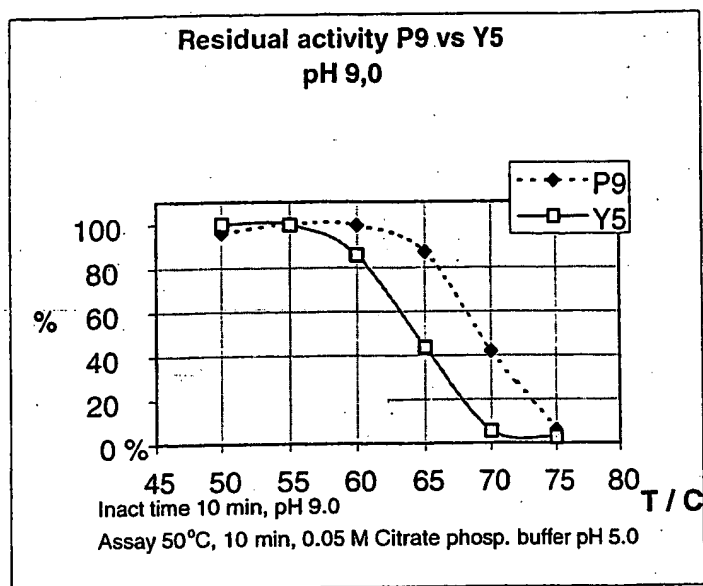


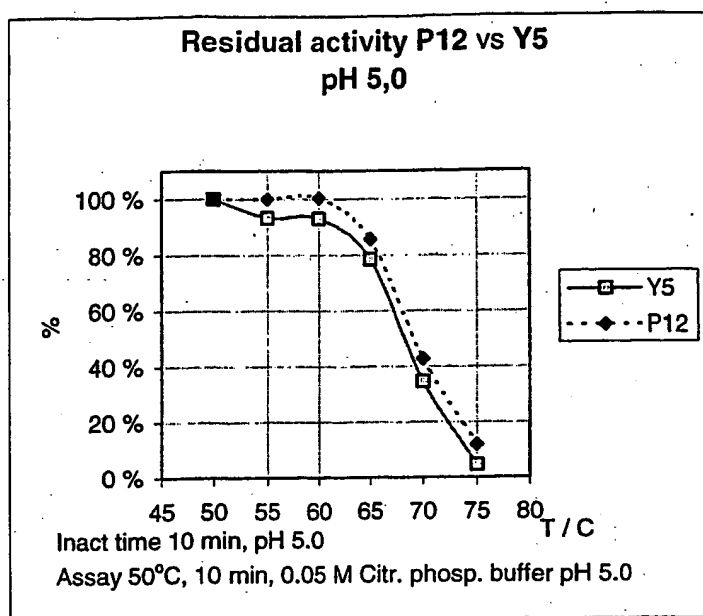
Figure 10.

Figure 11.

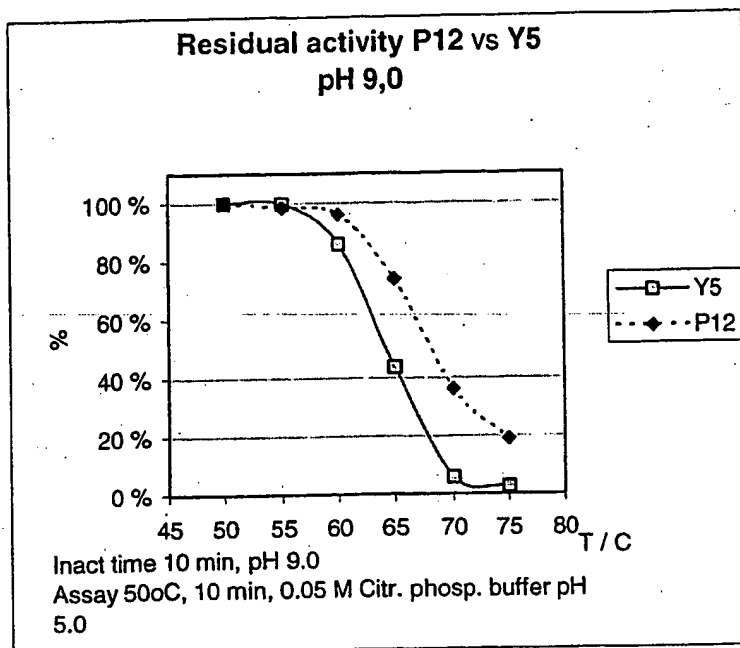


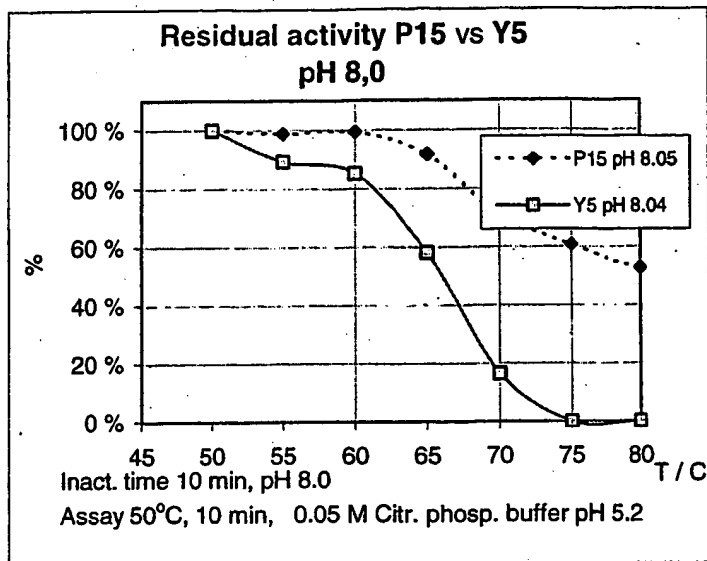
Figure 12.

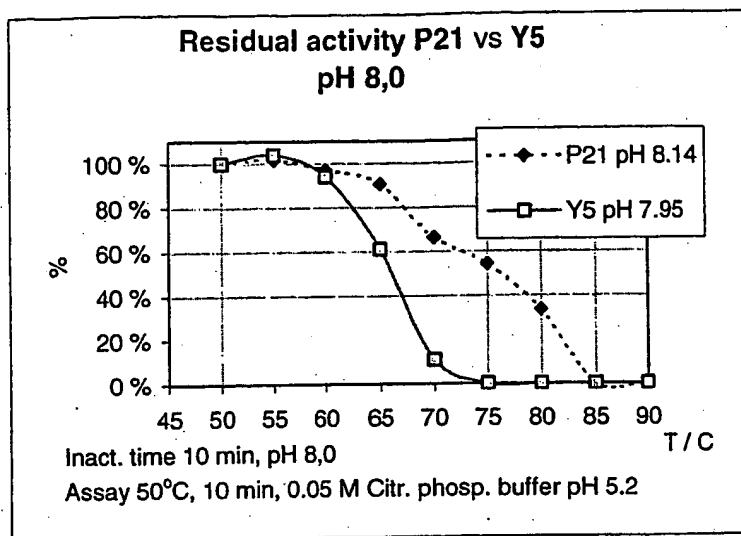
Figure 13.

Figure 14.

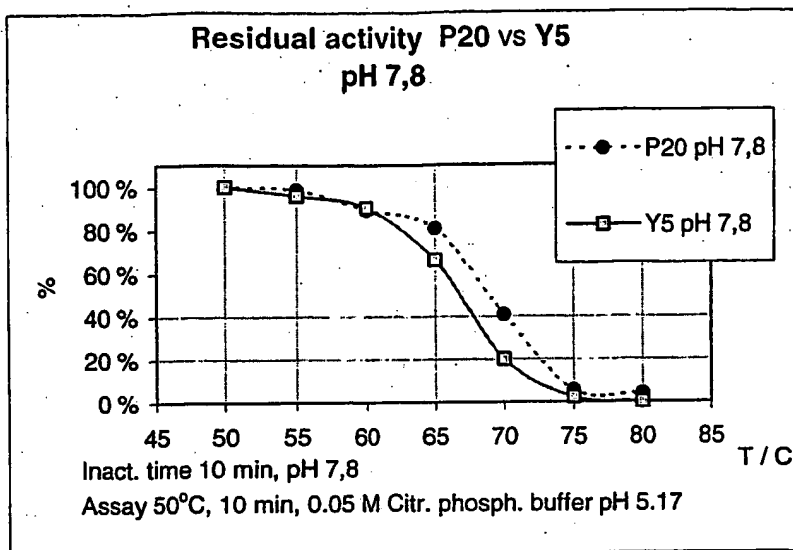


Figure 15.

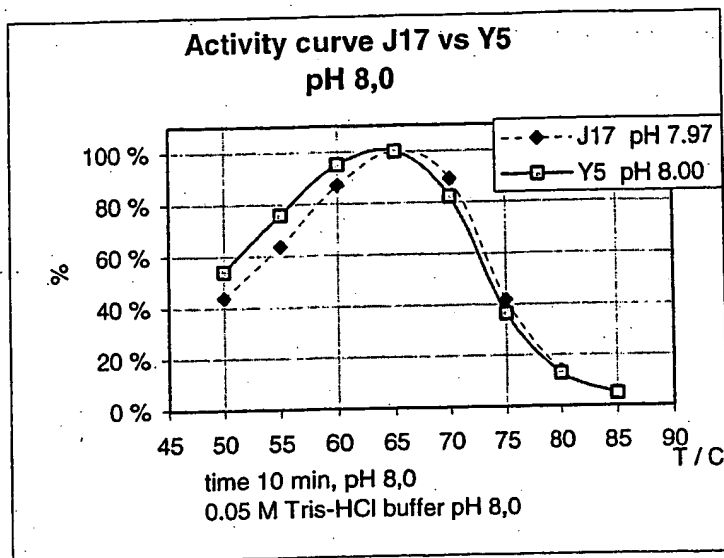


Figure 16.

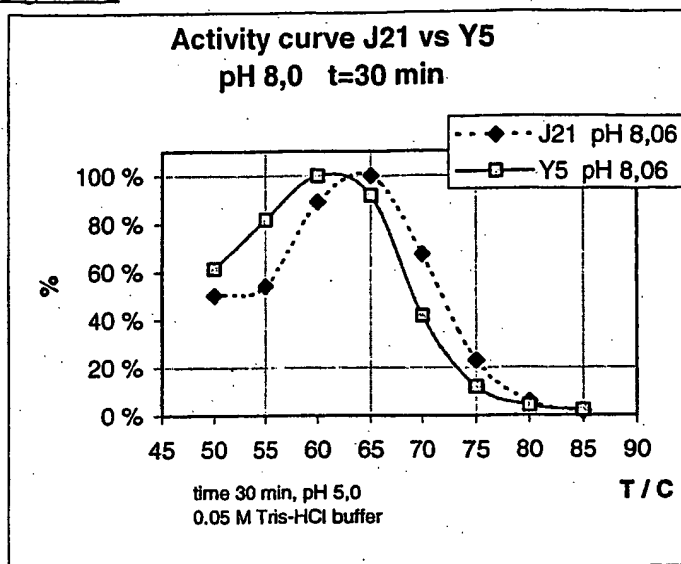


Figure 17

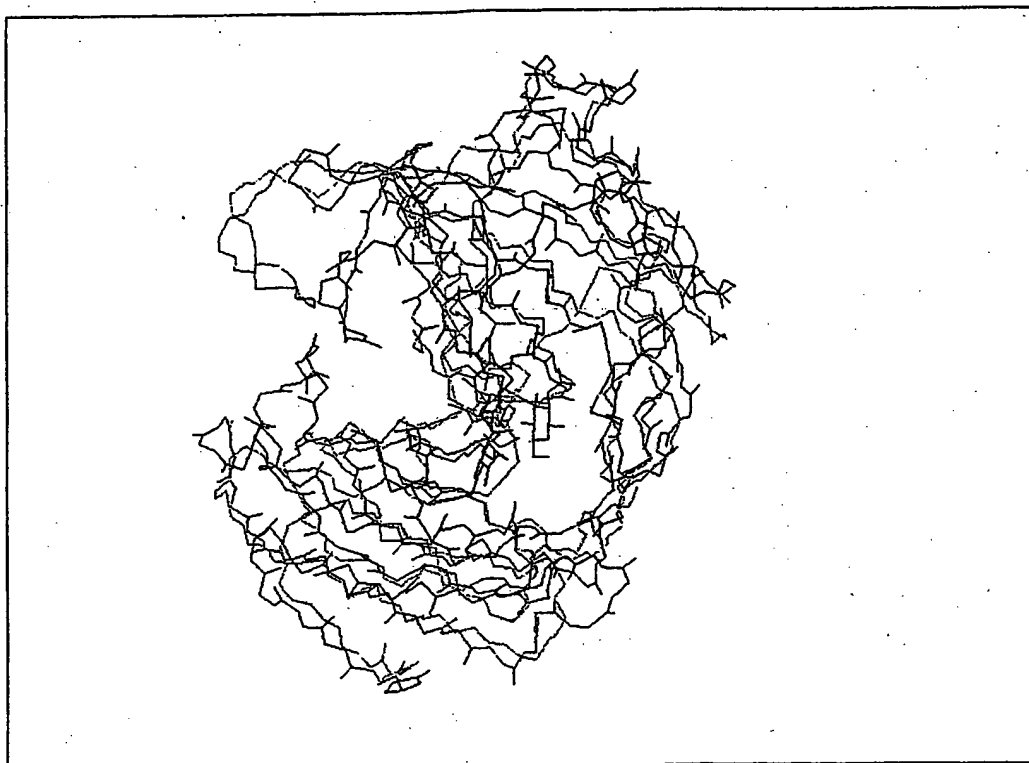


Figure 18

Trichoderma reesei Xyl II protein (high pl xylanase)
the full sequence, including signal and pro sequence

MVSFTSLLAGVAASGLAAPAAEVESVAVEKRTIQPGTGYNNGYFYSWNDHGHHGGVYTNPGGQGFVSNWSNSGNFVG
GKGWQPGTKNKVINFGSYNPNNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTS DGSVYDIYRTQRVNQPS
IIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQQGLTLGTM DYQIVAVEGYFSSGSASITVS (SEQ. ID NO: 1)

Trichoderma reesei XynII gene (high pl xylanase)
DNA from start codon to stop codon (includes a single intron)

ATGGTCTCCTTCACCTCCCTCCTCGCCGGCGTCCGCCCATCTCGGGCGTCTTGGCCGCTCCCGCCGCGAGGTCGAATC
CGTGGCTGTGGAGAGCGCCAGACGATTACGCCGCGCACGGCTACAACAACGGCTACTTCTACTCGTACTGGAACGATG
GCCACGGCGCGTGACGTACACCAATGGTCCCGGGCGAGTTCTCCGTCAACTGGTCCAACCTCGGGCAACTTTGTCTGGC
GGCAAGGGATGGCAGCCCGGCACCAAGAACAAAGTAAGACTACCTACTCTTACCCCTTTGACCAACACAGCACACACAA
TACAACACATGTGACTACCAATCATGGAATCGGATCTAACAGCTGTGTTTTCAAAAAAAGGGTCATCAACTTCTCGGGC
AGCTACAAACCCCAACGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTGATCGAGTACTACATCGTCTCGA
GAACCTTTGGCACCTACAACCCGTCACGGCGGCCCAAGCTGGCGAGGTCACTCCGACGGCAGCTCTACGACATTT
ACCGCACGCGCGGTCAACACGCGTCCATCATCGGCACCGCCACCTTTACCAAGTACTGGTCCGTCGCCGCAACCCAC
CGCTCGAGCGGCTCCGTCAACACGCGGAACCACTTCAACGCGTGGGCTCAGCAAGGCTGACGCTCGGGACGATGGATTA
CCAGATTGTTGCCGTGGAGGGTACTTTAGCTCTGGCTCTGCTTCCATCACCGTCAGCTAA (SEQ. ID NO: 2)

Figure 19

Trichoderma reesei EGL III protein (endoglucanase III)
the full sequence, including signal sequence

MKFLQVLPAALPAALQATSCDQWATFTGNGYTVSNLWLGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNVKSQNSQ
IAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVITYSGDYELMIWLKYGDIGPIGSSQGTNVNNGQSW
TLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFNYLRDNKGYNAAGQVYLSYQFGTEPFTGSGTLNVASWTASIN
(SEQ. ID NO: 3)

Trichoderma reesei EG III gene (endoglucanase III)
DNA from start codon to stop codon (includes two introns)

ATGAAGTTCCTTCAAGTCCTCCCTGCCCCTCATACCGGCCGCCCTGGCCAAACCAGCTGTGACCAGTGGGCAACCTTCAC
TGGCAACGGCTACACAGTCAGCAACAACCTTTGGGAGCATCAGCGGCTCTGGATTTGGCTGCGTGACGGCGGTATCGC
TCAGCGCGGGCCCTCCTGGCACGCAGACTGGCAGTGGTCCGGCGGCCAGAACACGTCAAGTCGTACCGAACTCTCAG
ATTGCCATTCCCAGAAAGAGACCGGTCAACAGCATCAGCAGCATGCCACCACTGCCAGCTGGAGCTACAGCGGGAGCAA
CATCCGCGCTAATGTTGCGTATGACTTGTTACCCGAGCCCAACCGAATCATGTACGTACTCGGGAGACTACGAACTCA
TGATCTGGTAAGCCATAAGAAGTGACCCCTCCTTGATAGTTTCGACTAACACATGCTTGAGGCTTGGCAAATACGGCGA
TATTGGGCCGATTGGGTCTCACAGGGAACAGTCAACGTCCGGTGGCCAGAGCTGGACGCTCTACTATGGCTACAACGGAG
CCATGCAAGTCTATTCTTTGTGGCCAGACCAACTACCACTACAGCGGAGATGTCAAGAACTTCTTCAATTATCTC
CGAGACAATAAAGGATACAACGCTGCAGGCCAATATGTTCTTAGTAAGTCAACCTCACTGTGACTGGGCTGAGTTTGTG
CAACGTTTGCTAACAAACCTTCGTATAGGCTACCAATTTGGTACCGAGCCCTTCACGGGCAGTGGAACTCTGAACGTCG
CATCCTGGACCGCATCTATCAACTAA (SEQ. ID NO: 4)

Figure 20

atggttgccctttccaggcctcatctgcgcctcacacgcatcggccagttactctggcgcgatggccccacagggccctggccctggagagcagtggtcaaacgtcacacagagcgtggcgcatgtacagcacttggtttctggaggtcacaaatgatcatcggcgcgtctgctagcatcaaatcagcaccaaaacttaccaaactggcgggacaagtcagcattctcagtggaactggcgtcttcacacactggcgtcttcacacactgggaaacactcaagatgactttgttggggcggttgggtggacgactggatctctggtaggagagactctcatattctggcactttgaaagcatctctggaccaaaagctctcttagtctcccatcaactttggcgcgcttttttaggtgtcaaacagcgggaactggccctgctttctgcttctatgggtggagcacaacaoccatgggttgagtactatcatatggagggacaacaacacataccagcacaggggttaccgtcacaagggggaaaccgtccacaggcgagcggacactttacacacatctggggggaataaccctggtcaacggggccttccatccacgggcacagggcaccgttcaaccagttacattctcgtggcggaactcggcccccacagggcaccagggggaaactgttactgtgcagaaaccacttcaatgacttggggccctcgcccttggcgccagatgaaactaccaggtttgtcgtcgtctggaaggcctgggggttgggttaggtgttctgtcctcacagaggtgtcagcaac

Xylanase I Amino Acid sequence

MVAFSSLCALTSIASTLAMPTGLEPSSVNVTERGMVDFVLGAHNDHRRRASINYDQNYQTGGQVSYSPSNTGFSVNVW
 N
 TQDDFVVGVGWTTGSSA.EDSSSFCTLKASSDQKLLVPSTLAALLVSTAELACFPSMAGAPTHWLSTTSWRITTTTQHR
 VPSREPSA TEPLTPSGRIPVSTSLPSAQRPSSTFP CGTRPGPAELL CRTTSM LGPRLACTLGR.TTRL SLSKAGVV
 VVLPHRVVSAT